

665022-06T5H200

Comparison of Mouse and Human TNF Family Related Proteins (TFRPs)

human	1	MSLLDFEISA	RRLEPRLSLG	SRDGGAVRQA	QPPAPMAARR	SQRRRGRRGE	50
mouse		
human	51	PGTALLVPLA	LGLGLALACL	GLLLAVVSLG	SRASLSAQEP	AQEELVAEED	100
mouse	V	LSLGLALACL	GLLLVVVSLG	SWATLSAQEP	SQEELTAEDR	
human	101	QDPSELNPQT	EESQDPAPFL	NRLVRPRRSA	PKGRKTRARR	AIAAHYEVHP	150
mouse		REPELNPQT	EESQDVVPFL	EQLVRPRRSA	PKGWKARPRR	AIAAHYEVHP	
human	151	RPGQDGAQAG	VDGTVSGWEE	ARINSSSPLR	YNRQIGEFIV	TRAGLYYLYC	200
mouse		RPGQDGAQAG	VDGTVSGWEE	TKINSSSPLR	YDRQIGELTV	IRAGLYYLYC	
human	201	QVHFDEGKAV	YLKLDLLVDG	VLALRCLEEF	SATAASSLGP	QLRLCQVSGL	250
mouse		QVHFDEGKAV	YLKLDLLVNG	VLALRCLEEF	SATAASSPGP	QLRLCQVSGL	
human	251	LALRPGSSLR	IRTLPWAHLK	AAPFLTYFGL	FQVH		284
mouse		LPLRPGSSLR	IRTLPWAHLK	AAPFLTYFGL	FQVH		

FIG. 1

An alignment of 10 human members of the TNF ligand family illustrating the variations in the length of the intracellular N-terminal domains and the stalk regions spacing the C-terminal receptor binding domain from the transmembrane region (beginning just before the first beta strand). The N terminus of human FasL has been truncated. The alignment weighs cysteine conservation heavily and due to the very poor homology in certain regions between some family members, many alternative alignments can be proposed varying in the details. The bars over the sequences indicate beta strand structures in TNF and LT with the nomenclature being that used by Eck and Sprang. Canonical N-linked glycosylation sites are underlined as are probable transmembrane sequences and the disulfide linked cysteines in TNF are marked with dots. Starred sequences are motifs useful in the recognition of TNF family members.

FIG. 2A

	A'	B'	B	C	D	E				
hTNF	RANALLAN	GVELRD	--NQ--	LIVPSEGLYLIY	--SQVLFKGGCPSTHVLTHHTISRLAVS----	--YQTKVN--	LLSAKYS-----	PCQRETPEGAEAK		
hLT- α	TDRAFLQD	--GFSLS--	NNS--	LLVPTSGIYFVYNISQWFSQKAY	--SPKAT--	SSPLYLAHEVQLFSSQYFFHVP--	LLSSQIQM----	VY--PGLQE-----		
hLT- β	KEQAFLT	--SGTQFSDAEG--	LAL	PDGLYLYLTYCLVGYRGRAPPGGDPQGRSVTLRSLYRAGGAYGPGTPELLLEGAETVTPVLDPARRQGYG----						
hFasL	YGIVLL	--SGVKYKK--	GG--	LVINETGLYFVY--	SKVYFRGQSCNNQPLSHKVMYRN----	SK----	YPQDL----	VMEGQM--	MSY--	CTTGQ-----
hTRP	RINSSPLRYNRQI	--GE--	FIVTRAGLYLY	--CQHFDEGKAVYLKDL	LLVDGLALRCLDEEFSATAASSLGPQLRL-----					CQVSGLL
hTRAIL	RSCHSFLSNLHLRN	--GE--	LVIHEKGFYIY	--SQTYFRQEEIKENTQDXQMVQIYKVTIS----	YDPI----	LLMKSARNS-----				CWSKDAEY
hCD27L	PALGRSFLHGPEL	--DKGQ--	LRIHRDGIYMWHI	--QVTLAI--	CSSTASRRHPTTLAVGICSPASRSIS-----	LLRLSFHQG-----				CTIV-----
hCD30L	G-----	ILHGVRYQD	--GN--	LVIQFPGLYPII	--CQLQFLVQ--	CPNNSVDLKLELLINKHIKK--	QALVT-----	VCESGMQFKHVYQNL	SQFL-----	
hCD40L	GYTMSNNLVTL	--ENGKQ--	LTVKRGLYIYA	--QVTF--	CSNREASSQAPFLASLCLKSPGRFERI-----	LLRAAN--	THSSAKPCGQSIH-----			
h4-1BBL	DGAGSSYLSQGLRYEEDK	KLAVNDS	PGLYVVFLELKLSPFT	TNTGKVVQGWVSLVLQAKP--	QVDDFDN-----	LAL-----	TVELF--	PCSMENKLVDRS		

	F	G	H
hTNP	P-WYEP	IYLG	VFQLEKGDRLSAEINR
hLT-α	P-WLHSMYHGA	FQLTQGDQLSTH	DGIPHLVL--SPS--TVFFGAPAL
hLT-β	PLWYTSV	GFGGLVQLRRGERV	VYNISHPDMVDFAR--GKT-FFGAVMVG
hPasL	-MWARSSYL	GAVFNLT	SADHLVYNVSEL--SLVNFEESQT-FFGLYKL
hTRP	ALRPGSSLR	IRTL	PWAHLKAAPFL-----T-YFGLFQVH
hTRAIL	--GLYSIYQGG	IFELKENDRI	FVSVTNEHLIDMDHEA--S-FFGAPFLVG
hCD27L	-SORLTP	PLARGDTL	CTNLGTLLPSR-NTDE-----T-FFGVQWVRP
hCD30L	--LDYLQVNTT	ISVNVDTFQY	IDTST-FPLE-NVL-----S-IFLYSNSD
hCD40L	-----LGGV	FELQ	PGASVFNVTDP
hCD40L			PSQVSHG-----TGFTS-FGLLKL
h4-1BBL	--WSQLLL	LLKAGHRLSVGL	RAYLHGAQDAYRDWELSYPNNTIS-FGLFLVKPDNPWE

FIG. 2B

APPROVED	FIG.
BY	SUBCLASS
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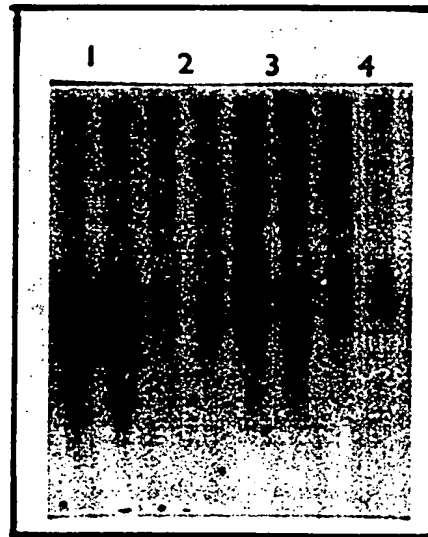
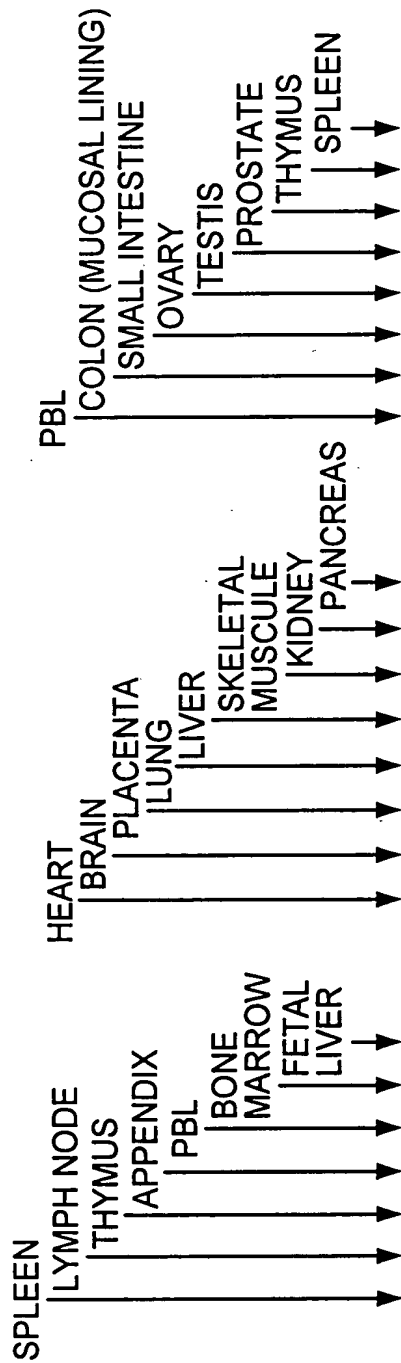
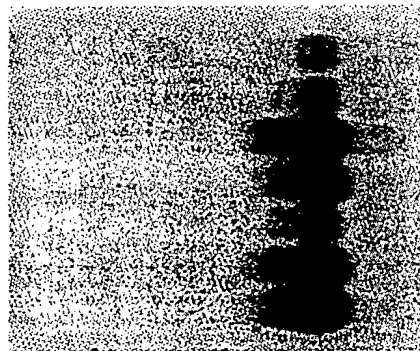


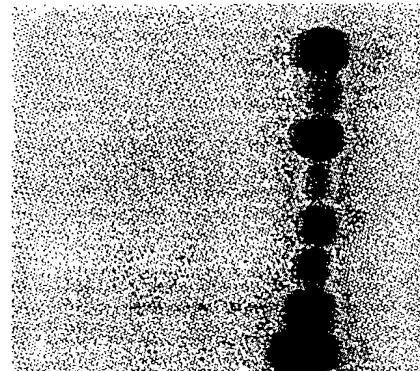
FIG. 3



7.5
4.4
2.4
1.35



— — — — —



9.5
7.5
4.4
2.4
1.35

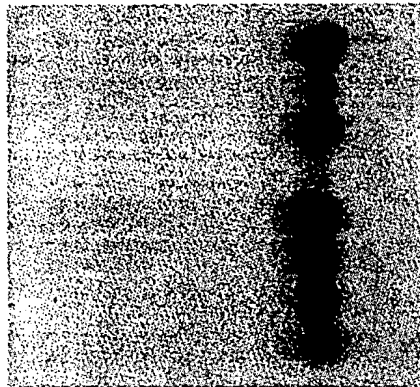


FIG. 4

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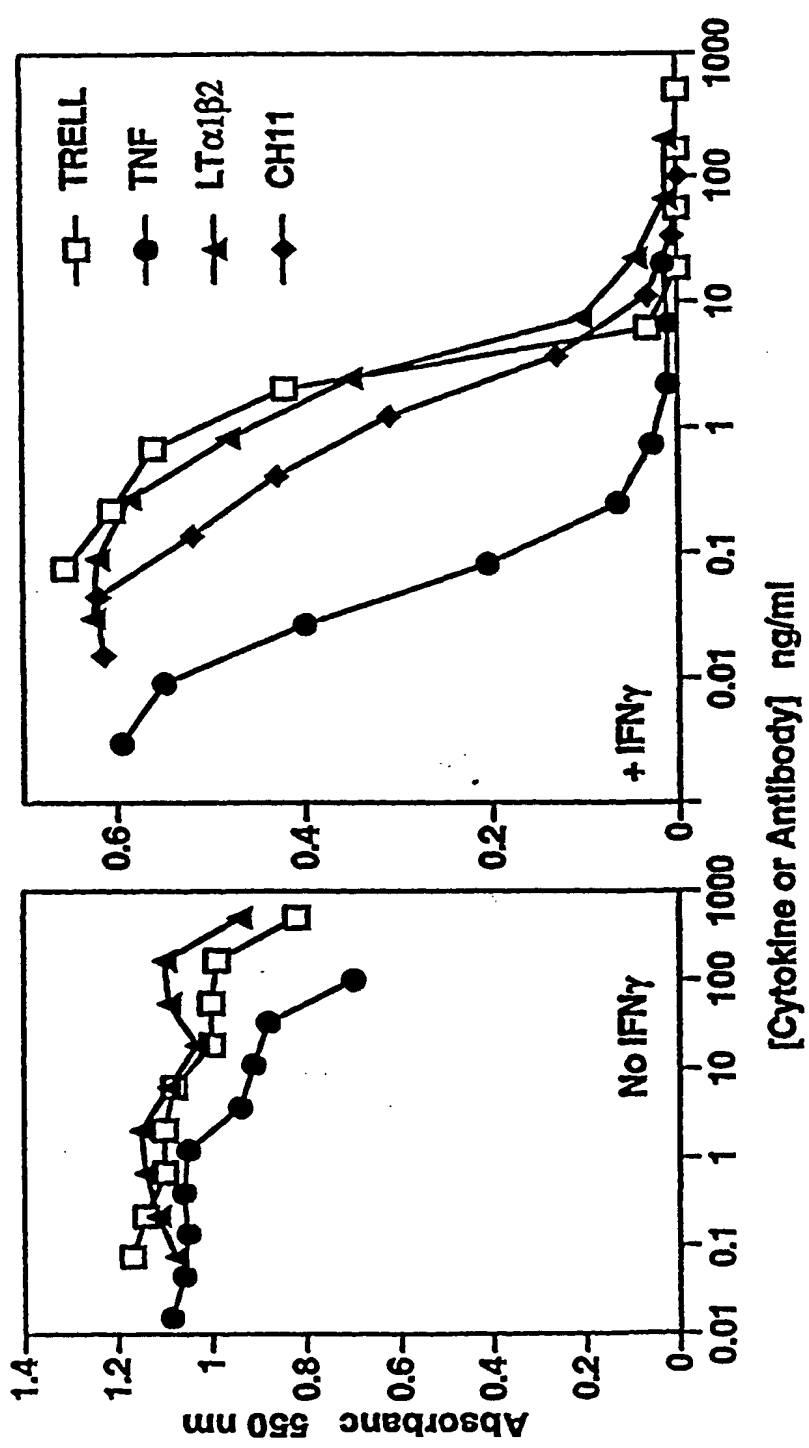


FIG. 6A

